

SEARCH REQUEST FORM

7-217

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: _____
Searcher: Shirley
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other

STIC-Biotech/ChemLib

From: Teng, Sally
To: STIC-Biotech/ChemLib
Subject: 08/426,509
Date: Thursday, July 10, 1997 10:17AM

1-277

Interference Search

Please search SEQ ID NO: 1-6

31	75	16.2	256	17	R85919	Human GRB-3.	1.04e+01
32	75	16.2	536	8	R39706	Human pp60 c-src prot	1.04e+01
33	74	15.9	501	18	W03760	Mullerian inhibiting	1.28e+01
34	74	15.9	505	8	R41921	MISR2A/MISR2B.	1.28e+01
35	74	15.9	505	10	R55369	Human Activin recepto	1.28e+01
36	74	15.9	505	13	R70240	Serine/threonine kina	1.28e+01
37	74	15.9	505	10	R55373	Mouse Activin recepto	1.28e+01
38	71	15.3	1290	15	R90583	Phospholipase C-gamma	2.41e+01
39	70	15.1	128	13	R64261	MAB L243 light chain	2.96e+01
40	70	15.1	128	12	R64231	MAB L243 VL region.	2.96e+01
41	69	14.9	509	16	R94601	TAR-1 polypeptide.	3.64e+01
42	68	14.7	86	11	R56775	Human anti-haemophili	4.46e+01
43	68	14.7	2332	2	P71728	Factor VIII:c variant	4.46e+01
44	68	14.7	2351	3	P60741	Sequence of human fac	4.46e+01
45	68	14.7	2351	13	R78223	Human Factor-VIII:c.	4.46e+01

ALIGNMENTS

RESULT 1

ID R71129 standard; Protein: 64 AA.
AC R71129;
DT 27-OCT-1995 (first entry)
DE SH3 domain of cytoplasmic tyrosine kinase.
KW cytoplasmic; tyrosine kinase; blood; cell differentiation;
KW screening; anticancer agent; SH3; src homology domain.
OS Homo sapiens.
PN W09506113-A.
PD 02-MAR-1995.
PF 25-AUG-1994; J01411.
PR 25-AUG-1993; JP-210403.
PR 29-MAR-1994; JP-058553.
PA (ASAH) ASahi KASEI KOGYO KK.
PI Sakano S;
DR WPI; 95-106842/14.
DR N-PSDB; 084888.
PT Cytoplasmic tyrosine kinase and antibody recognising it - for
PT screening chemical substances for tyrosine kinase inhibitory or
PT activating activity for use as cancer therapy
PS Claim 1; Page 38; 58pp; English.
CC A cytoplasmic tyrosine kinase which has enhanced expression in
CC connection with blood cell differentiation has been isolated from the
CC human UT-7 blood cell line. This sequence comprises the SH3 (src
CC homology) domain of the enzyme (residues 7-70 of R71132; residues
CC 48-111 of R71133). The DNA sequences and antibodies raised against
CC the enzyme, are useful for screening agents for inhibiting or activating
CC activity on the tyrosine kinase, for use as anticancer agents.
SQ Sequence 64 AA;

Query Match 100.0%; Score 464; DB 13; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.20e-44;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 apgtqcitkcehtrpkpgelafkrkgdvvtileacenksyrvkhhtsgqegllaagalre 60
|||||
Qy 48 APGTQCITKCENTRPKPGELAFKRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRE 107
Db 61 real 64
||||
Qy 108 REAL 111

RESULT 2

ID R71132 standard; Protein: 466 AA.
AC R71132;
DT 27-OCT-1995 (first entry)

Run on: Mon Feb 3 16:52:10 1997; MasPar time 2.72 Seconds
241.839 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-2
Description: (48-111) from US08426509.pep (1 of 4)
Perfect Score: 464
Sequence: 1 APGTQCITKCEHTRPKPGEL.....HTSGQEGLLAAGALRREAL 64

Scoring table: PAM 150
Gap 11

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 25.991; Variance 87.600; scale 0.297

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description	Pred. No.
1	464	100.0	64 13	R71129	SH3 domain of cytopl	1.20e-44
2	464	100.0	466 13	R71132	N-terminal truncated	1.20e-44
3	464	100.0	507 13	R71133	Cytoplasmic tyrosine k	1.20e-44
4	460	99.1	507 15	R84181	Megakaryocyte kinase	3.71e-44
5	113	24.4	217 17	R85918	Human GRB-2.	1.83e-03
6	112	24.1	176 13	R71943	Grb3-3 protein.	2.32e-03
7	104	22.4	217 15	R84636	Grb2 protein.	1.55e-02
8	100	21.6	620 17	R94535	ITK tyrosine kinase.	3.93e-02
9	98	21.1	821 7	R35451	Mouse eps8.	6.25e-02
10	95	20.5	659 17	R94534	BTK tyrosine kinase.	1.25e-01
11	90	19.4	317 5	R26061	Growth Factor Recepto	3.88e-01
12	87	18.8	212 10	R53543	Thyroid hormone recep	7.60e-01
13	85	18.3	303 17	R77439	Mouse CRKL protein.	1.19e+00
14	84	18.1	466 13	R71910	Erythroid p55.	1.48e+00
15	81	17.5	475 6	R31046	Rat D1B dopamine rece	2.86e+00
16	80	17.2	963 18	R84082	Thermostable enzyme I	3.55e+00
17	78	16.8	78 9	R46684	Fragment 273-351 of G	5.47e+00
18	78	16.8	516 9	R46685	Peptide P9 inhibits r	5.47e+00
19	78	16.8	533 8	R39705	Chicken pp60 c-src pr	5.47e+00
20	78	16.8	844 5	R25671	Mouse vav proto oncog	5.47e+00
21	78	16.8	870 11	R59924	Human GAP protein.	5.47e+00
22	78	16.8	1047 5	R25336	Lambda clone 101 prot	5.47e+00
23	78	16.8	1047 2	R06328	Sequence of full leng	5.47e+00
24	78	16.8	1047 2	R11137	GAP6 encoded by lambd	5.47e+00
25	77	16.6	298 15	R84183	Megakaryocyte kinase	6.78e+00
26	77	16.6	390 15	R83825	p47(phox) protein.	6.78e+00
27	77	16.6	505 15	R85929	Protein tyrosine-kina	6.78e+00
28	77	16.6	505 8	R41941	PTK gene LpTK-2 prod.	6.78e+00
29	76	16.4	61 11	R60993	Fragment of p56lck co	8.40e+00
30	76	16.4	1713-13	R70148	Deduced sequence of c	8.40e+00

DE N-terminal truncated cytoplasmic tyrosine kinase.
KW cytoplasmic; tyrosine kinase; blood; cell differentiation;
KW screening; anticancer agent; SH3; src homology domain.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 7..70
FT /note= "SH3 domain"
FT Domain 81..155
FT /note= "SH2 domain"
FT Domain 192..438
FT /note= "tyrosine kinase domain"
PN W09506113-A.
PD 02-MAR-1995.
PF 25-AUG-1994; J01411.
PR 25-AUG-1993; JP-210403.
PR 29-MAR-1994; JP-058553.
PA (ASAH) ASAMI KASEI KOGYO KK.
PI Sakano S;
DR WPI; 95-106842/14.
DR N-PSDB; 084888.
PT Cytoplasmic tyrosine kinase and antibody recognising it - for
PT screening chemical substances for tyrosine kinase inhibitory or
PT activating activity for use as cancer therapy
PS Claim 1; Page 40-42; 58pp; English.
CC A cytoplasmic tyrosine kinase which has enhanced expression in
CC connection with blood cell differentiation has been isolated from the
CC human UT-7 blood cell line. This sequence comprises an N-terminal
CC truncated fragment of the enzyme (residues 42-507 of R71133). The DNA
CC sequences and antibodies raised against the enzyme, are useful for
CC screening agents for inhibiting or activating activity on the tyrosine
CC kinase, for use as anticancer agents.
SQ Sequence 466 AA;

Query Match 100.0%; Score 464; DB 13; Length 466;
Best Local Similarity 100.0%; Pred. No. 1.20e-44;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 apgtqcitkcehtprkpgelafkrkgdvvtileacenksyrvkhhtsgqegllaagalre 66
|||||
Qy 48 APGTQCITKCEHTPRKPGELAFKRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRE 107
Db 67 real 70
||||
Qy 108 REAL 111

RESULT 3
ID R71133 standard; Protein; 507 AA.
AC R71133;
DT 27-OCT-1995 (first entry)
DE Cytoplasmic tyrosine kinase.
KW cytoplasmic; tyrosine kinase; blood; cell differentiation;
KW screening; anticancer agent; SH3; src homology domain.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 48..111
FT /note= "SH3 domain"
FT Domain 122..196
FT /note= "SH2 domain"
FT Domain 233..478
FT /note= "tyrosine kinase domain"
PN W09506113-A.
PD 02-MAR-1995.
PF 25-AUG-1994; J01411.
PR 25-AUG-1993; JP-210403.
PR 29-MAR-1994; JP-058553.

PA (ASAH) ASAH KASEI KOGYO KK.
 PI Sakano S;
 DR WPI; 95-106842/14.
 DR N-PSDB; 084888.
 PT Cytoplasmic tyrosine kinase and antibody recognising it - for
 PT screening chemical substances for tyrosine kinase inhibitory or
 PT activating activity for use as cancer therapy
 PS Claim 1; Page 42-44; 58pp; English.
 CC A cytoplasmic tyrosine kinase which has enhanced expression in
 CC connection with blood cell differentiation has been isolated from the
 CC human UT-7 blood cell line. The DNA sequences and antibodies raised
 CC against the enzyme, are useful for screening agents for inhibiting or
 CC activating activity on the tyrosine kinase, for use as anticancer agents.
 SQ Sequence 507 AA;

Query Match 100.0%; Score 464; DB 13; Length 507;
 Best Local Similarity 100.0%; Pred. No. 1.20e-44;
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 48 apgtqcitkcehtrpkpgelafkrkgdvvtileacenkswyrvkhhtsgqegllaagalre 107
 |||
 Qy 48 APGTQCITKCEHTRPKPGELAFKRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRE 107

 Db 108 real 111
 |||
 Qy 108 REAL 111

RESULT 4

ID R84181 standard; Protein; 507 AA.
 AC R84181;
 DT 26-MAR-1996 (first entry)
 DE Megakaryocyte kinase MKK1.
 KW Megakaryocyte kinase-1; MKK1; cytoplasmic tyrosine kinase;
 KW cellular signal transduction; leukaemia; thrombocytopenia.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 48..111
 FT /label= SH3_domain
 FT Domain 122..196
 FT /label= SH2_domain
 FT Domain 233..478
 FT /label= Catalytic_domain
 PN WD9529185-A1.
 PD 02-NOV-1995.
 PF 24-APR-1995; U05008.
 PR 22-APR-1994; US-232545.
 PR 21-APR-1995; US-426509.
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PA (SUGE-) SUGEN INC.
 PI Gishizky M, Sures I, Ullrich A;
 DR WPI; 95-382959/49.
 DR N-PSDB; T00616.
 PT New poly:nucleotide(s) encoding megakaryocyte tyrosine kinase(s) -
 PT used to develop prods. for the treatment and diagnosis of kinase
 PT related signal transduction abnormalities.
 PS Claim 15; Fig 1A-C; 82pp; English.
 CC Human megakaryocyte kinase MKK1 (R84181) is a 58 kDa cytosolic
 CC tyrosine kinase showing 54% homology with csk. It appears to play
 CC a regulatory role in the growth and differentiation of
 CC megakaryocytes and perhaps neural tissues. Recombinant MKK1 can be
 CC produced in host cells by expression of encoding cDNA (T00616), and
 CC used in the treatment and diagnosis of e.g. leukaemia and
 CC thrombocytopenia.
 SQ Sequence 507 AA;

Query Match 99.1%; Score 460; DB 15; Length 507;
Best Local Similarity 98.4%; Pred. No. 3.71e-44;
Matches 63; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 48 apgtqcitkcehtrpkpgelafkrkgdvvtileacenksyrvkhhtsgeegllaagalre 107
|||||
Qy 48 APGTQCITKCEHTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSGEGLLAAGALRE 107

Db 108 real 111
||||
Qy 108 REAL 111

RESULT 5

ID R85918 standard; Protein: 217 AA.
AC R85918;
DT 16-MAY-1996 (first entry)
DE Human GRB-2.
KW GRB-2; growth factor receptor bound; tyrosine kinase; regulation;
KW cell growth; cellular metabolism; screening; signal transduction;
KW cancer; diabetes; CORT technique; cloning of receptor targets.
OS Homo sapiens.
PN W09524426-A1.
PD 14-SEP-1995.
PF 13-MAR-1995; U03385.
PR 11-MAR-1994; US-208887.
PA (UUNY) UNIV NEW YORK STATE.
PI Margolis BL, Schlessinger J, Skolnik EY;
DR WPI; 95-328235/42.
DR N-PSDB; T07167.
PT DNA encoding tyrosine kinase-binding proteins - used to screen
PT agents capable of modulating cell growth or cellular metabolism
PS Disclosure; Fig 26A-C; 215pp; English.
CC Using a new cloning technique, CORT (cloning of receptor targets)
CC several new tyrosine kinase (TK) binding proteins were isolated. Growth
CC factor receptor bound proteins GRB-1, GRB-2, GRB-3, GRB-4, GRB-7 and
CC GRB-10 were isolated using this method. This sequence represents GRB-2.
CC The proteins bind to a tyrosine-phosphorylated domain of a eukaryotic
CC TK. GRB proteins can be used for screening agents which are capable
CC of modulating cell growth that occurs via signal transduction through
CC TKs. Such agents can be used to prevent or inhibit cell growth or to
CC counteract tumour development. GRB proteins are also useful for
CC identifying susceptibility to diseases associated with alterations in
CC cellular metabolism mediated by TK pathways e.g. cancer and diabetes.
SQ Sequence 217 AA;

Query Match 24.4%; Score 113; DB 17; Length 217;
Best Local Similarity 33.3%; Pred. No. 1.83e-03;
Matches 12; Conservative 11; Mismatches 11; Indels 2; Gaps 2;

Db 4 iakdyfkataddelsfkrkdilvlnecdqn-wyk 38
|:| : |||::||:: :| | |: : ||:
Qy 54 ITKCEHTRPKPGELAFRKGDVVTIL-EACENKSWYR 88

RESULT 6

ID R71943 standard; Protein: 176 AA.
AC R71943;
DT 17-OCT-1995 (first entry)
DE Grb3-3 protein.
KW Grb3-3; cancer; apoptosis; AIDS; gene therapy.
OS Homo sapiens.
PN W09507981-A.
PD 23-MAR-1995.
PF 09-MAY-1994; F00542.
PR 15-SEP-1993; FR-010971.

Query Match 24.1%; Score 112; DB 13; Length 176;
Best Local Similarity 30.6%; Pred. No. 2.32e-03;
Matches 11; Conservative 12; Mismatches 11; Indels 2; Gaps 2;

RESULT 7

Query Match 22.4%; Score 104; DB 15; Length 217;
Best Local Similarity 27.8%; Pred. No. 1.55e-02;
Matches 10; Conservative 13; Mismatches 11; Indels 2; Gaps 2;

Db 4 iakydfkataddelsfkradilkvlnqecdqn-wyk 38
|:| : ||:|::|:: :| : |: : ||:
Qy 54 ITKCENTRPPKPGELAFRKGDVVTIL-EACENKSWYR 88

RESULT 8

ID R94535 standard; Protein; 620 AA.
AC R94535;
DT 10-JUL-1996 (first entry)
DE ITK tyrosine kinase.
KW Cytoplasmic tyrosine kinase; BMX; haematopoietic cell;
KW cell growth; cell proliferation; tumour; diagnosis; therapy; ITK.
OS Mus musculus.
PN W09611275-A1.
PD 18-APR-1996.
PF 09-OCT-1995; F10555.
PR 07-OCT-1994; US-320432.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI Alitalo K;
DR WPI; 96-209856/21.
PT Cytoplasmic tyrosine kinase BMX and related DNA - useful to
PT stimulate haematopoietic cell growth.
PS Disclosure; Page 23-25; 40pp; English.
CC Cytoplasmic tyrosine kinase ITK (R94535) is selectively expressed
CC at certain stages of T-cell development. The sequences of ITK
CC and 2 other members of a newly-identified non-receptor tyrosine
CC kinase family, BTK (R94534) and TEC (R94536), and of the
CC Drosophila Src28C tyrosine kinase (R94538), were compared with
CC that of novel cytoplasmic tyrosine kinase BMX (see also R94533).
CC Close homology was found.
SQ Sequence 620 AA;

Query Match 21.6%; Score 100; DB 17; Length 620;
Best Local Similarity 29.1%; Pred. No. 3.93e-02;
Matches 16; Conservative 16; Mismatches 21; Indels 2; Gaps 2;

Db 177 ialydyqtndpqelalrrneeyclldsseih-wurvqdr-nghegyvpssylvek 229
|: : | |||:|: : :||: | || : :|:| :||: | :|
Qy 54 ITKCENTRPPKPGELAFRKGDVVTILEACENKSWYRVKHTSGEGLLAAGALRER 108

RESULT 9

ID R35451 standard; Protein; 821 AA.
AC R35451;
DT 25-AUG-1993 (first entry)
DE Mouse eps8.
KW Epidermal growth factor receptor; EGFR-pathway substrate; eps;
KW tyrosine kinase receptor; TKR; SH2; SH3; mitogenesis.
OS Mus musculus.
PN U57935311-A.
PD 01-APR-1993.
PF 25-AUG-1992; 935311.
PR 25-AUG-1992; US-935311.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
PI Di Fiore PP, Fazioli F;
DR WPI; 93-159477/19.
DR N-PSDB; 040730.
PT Epidermal growth factor receptor substrate, eps 8 - used to
PT enhance mitogenic response of cells to epidermal growth factor
PS Disclosure; Page 30-37; 40pp; English.
CC Eps8 is a novel EGFR substrate. The protein bears the
CC characteristic signatures of TKR substrates including SH2 and
CC SH3 domains. Eps8 is involved in the transduction of mitogenic
CC signals and it can be used to enhance the mitogenic response of
CC cells to EGF.
SQ Sequence 821 AA;

Query Match 21.1%; Score 98; DB 7; Length 821;
Best Local Similarity 27.5%; Pred. No. 6.25e-02;
Matches 14; Conservative 18; Mismatches 16; Indels 3; Gaps 2;

Db 537 skydfvarnsselsvskddvleild--drrquwkvrrn-asgdsgfvppnil 584
:| : :||| : ||| ||| : : | :||| :||| :||| :
Qy 55 TKCENTRPKPGELAFRKGDDVVTILEACENKSWYRVKHHTSGQEGLLAAGAL 105

RESULT 10

ID R94534 standard; Protein; 659 AA.
AC R94534;
DT 10-JUL-1996 (first entry)
DE BTK tyrosine kinase.
KW Cytoplasmic tyrosine kinase; BMX; haematopoietic cell;
KW cell growth; cell proliferation; tumour; diagnosis; therapy; BTK.
OS Mus musculus.
FH Key Location/Qualifiers
FT Domain 1..219
FT /label= N-terminal_region
FT /note= "the N-terminal region contains the
FT pleckstrin homology region consisting
FT of a 7-strand antiparallel beta-sheet"
FT Domain 220..272
FT /label= SH3_domain
FT Domain 281..336
FT /label= SH2_domain
FT Domain 407..644
FT /label= Tyrosine-kinase_domain
FT Binding_site 408..430
FT /label= ATP-binding_region
FT Modified_site 551
FT /label= Autophosphorylation_site
PN W09611275-A1.
PD 18-APR-1996.
PF 09-OCT-1995; F10555.
PR 07-OCT-1994; US-320432.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI Alitalo K;
DR WPI; 96-209856/21.
PT Cytoplasmic tyrosine kinase BMX and related DNA - useful to
PT stimulate haematopoietic cell growth.
PS Disclosure; Page 21-23; 40pp; English.
CC Cytoplasmic tyrosine kinase BTK (R94534) is selectively expressed
CC at certain stages of B-cell development. The sequences of BTK
CC and 2 other members of a newly-identified non-receptor tyrosine
CC kinase family, ITK (R94535) and TEC (R94536), and of the
CC Drosophila Src28C tyrosine kinase (R94538), were compared with
CC that of novel cytoplasmic tyrosine kinase BMX (see also R94533).
CC Close homology was found.
SQ Sequence 659 AA;

Query Match 20.5%; Score 95; DB 17; Length 659;
Best Local Similarity 36.2%; Pred. No. 1.25e-01;
Matches 17; Conservative 11; Mismatches 17; Indels 2; Gaps 2;

Db 229 nandlqlrkqgdeyfilees-nlpwrrard-kngqegypsnvyteae 273
: :| :||| ||| | :| | : :||| :||| :||| :
Qy 63 KPGELAFRKGDDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRERE 109

RESULT 11

ID R26061 standard; Protein; 317 AA.
AC R26061;
DT 02-FEB-1993 (first entry)

DE Growth Factor Receptor Bound protein GRB-2 partial sequence.
KW Tyrosine phosphorylation; epidermal growth factor receptor; EGFR;
KW src homology domain; SH2; SH3.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 30
FT /note= "start of SH2 domain"
FT Domain 133
FT /note= "start of SH3 domain"
FT Misc_difference 183
FT /note= "corresponds to CNG codon,
FT where N is unknown"
FT Misc_difference 184
FT /note= "corresponds to TGA codon"
FT Misc_difference 196
FT /note= "corresponds to TAA codon"
FT Misc_difference 199
FT /note= "corresponds to TGA codon"
FT Misc_difference 215
FT /note= "corresponds to TGA codon"
FT Misc_difference 231
FT /note= "corresponds to TGA codon"
FT Misc_difference 202
FT /note= "corresponds to TAA codon"
FT Misc_difference 299
FT /note= "corresponds to TGA codon"
FT Misc_difference 301
FT /note= "corresponds to TAA codon"
FT Misc_difference 302
FT /note= "corresponds to TAA codon"
FT Misc_difference 315
FT /note= "corresponds to TAG codon"
PN W09213001-A.
PD 06-AUG-1992.
PF 17-JAN-1992; U00434.
PR 18-JAN-1991; US-643237.
PA (UUNY) UNIV NEW YORK STATE.
PI Margolis BL, Schlessinger J, Skolnik EY;
DR WPI; 92-284605/34.
DR N-PSDB; 027255.
PT Probe from tyrosine-phosphorylated portion of receptor tyrosine
PT kinase - used for detection of proteins capable of binding to
PT receptors, useful for e.g. identifying susceptibility to cancer
PT and diabetes
PS Claim 18; Fig 16; 86pp; English.
CC The GRB-2 partial coding sequence was isolated from human brain stem
CC lambda gt11 expression library by screening with tyrosine
CC phosphorylated C-terminal tail of the EGF Receptor. The amino acid
CC sequence deduced from the nucleotide sequence (the "ORF" includes
CC several nonsense codons !) contains unique SH2 and SH3 domains.
CC See also 027254.
SQ Sequence 317 AA;

Query Match 19.4%; Score 90; DB 5; Length 317;
Best Local Similarity 36.4%; Pred. No. 3.88e-01;
Matches 8; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Db 143 gelgfrngdfihvmdnsdpnw 164
|||:||| : :: : : |
Qy 65 GELAFRKGDVVTILEACENKSW 86

RESULT 12
ID R53543 standard; protein; 212 AA.
AC R53543;
DT 21-FEB-1995 (first entry)

DE Thyroid hormone receptor-interacting protein - S410a
 KW nuclear thyroid hormone interacting proteins; TR; JL1; JL2; S410a;
 KW transcriptional coactivator; treatment; diagnosis; SH3 domains;
 KW thyroid related disorders; modulation; thyroid hormone receptor;
 KW nuclear hormone receptor; isolation.
 OS Chimeric Homo sapiens.
 OS Chimeric Bacterial sp.
 FH Key Location/Qualifiers
 FT Misc_difference 116
 FT /note= "stop codon encoded by TGA"
 PN W09410338-A.
 PD 11-MAY-1994.
 PF 29-OCT-1993; U10443.
 PR 30-OCT-1992; US-969136.
 PA (GEHO) GEN HOSPITAL CORP.
 PI Lee JW, Moore DD;
 DR WPI; 94-199808/24.
 PT Nuclear hormone receptor interacting polypeptides, esp. thyroid
 PT hormone=interacting proteins (TRs) - for identifying proteins
 PT useful in treatment and diagnosis of thyroid related disorders by
 PT inoculating thyroid hormone receptor activity
 PS Claim 21; Page 50-51; 105pp; English.
 CC This sequence shows the partial amino acid sequence of S410a
 CC (containing a SH3 domain), a thyroid hormone (TR) interacting protein.
 CC TR-interacting proteins physically associate with thyroid hormone
 CC receptor. Nearly all the fusion cDNAs showed very strong dependence
 CC on hormone activation. The proteins can be used in an in vivo trap
 CC system for the isolation of proteins which associate with any nuclear
 CC hormone receptor. The proteins and Abs may be used to treat or diagnose
 CC thyroid disorders, and to modulate thyroid hormone receptor activity.
 SQ Sequence 212 AA;

Query Match 18.8%; Score 87; DB 10; Length 212;
 Best Local Similarity 22.0%; Pred. No. 7.60e-01;
 Matches 13; Conservative 20; Mismatches 25; Indels 1; Gaps 1;

Db 54 spighcvaighfegssegtsnaegedlsneedkgdgwtrvrkegg-egyvptsytr 111
 :| :|:: :|:: |: :::| :| ||:: :| || ::: ||
 Gg 48 APTGTCITKCEHTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSCQEGLLAAGALR 106

RESULT 13

ID R77439 standard; Protein; 303 AA.
 AC R77439;
 DT 21-JUL-1996 (first entry)
 DE Mouse CRKL protein.
 KW Mouse CRKL protein; tyrosine phosphorylation; diagnosis;
 KW chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
 KW Philadelphia chromosome; BCL; ABL; treatment.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT Binding_site
 FT Domain 9..103
 FT /note= "SH2 domain"
 FT Domain 131..179
 FT /note= "N-terminal SH3 domain"
 FT Modified_site 193..210
 FT /note= "tyrosine phosphorylation site"
 FT Domain 238..290
 FT /note= "C-terminal SH3 domain"
 PN W09531545-A2.
 PD 23-NOV-1995.
 PF 12-MAY-1995; U05957.
 PR 13-MAY-1994; US-242513.
 PA (CHIL-) CHILDRENS HOSPITAL LOS ANGELES.
 PI Groffen JH, Heisterkamp NC, Ten Hoeve J;

DR WPI: 96-010931/01.
DR N-PSDB: T04144.
PT Diagnosis of tyrosine phosphorylated CRKL protein cancers - by
PT detecting increased level of CRKL protein or CRKL binding protein,
PT also compsns. for treating chronic myelogenous leukaemia.
PS Claim 37; Fig 10b; 74pp; English.
CC The mouse CRKL protein may be used in the diagnosis of Philadelphia
CC chromosome-positive leukaenias. For example, since CRKL is clearly
CC tyrosine-phosphorylated in chronic myelogenous leukaemia and
CC Philadelphia chromosome (Ph)-positive acute lymphoblastic leukaemia
CC patients expressing the BCR/ABL protein, but not in BCR-ABL-negative
CC peripheral blood cells, tyrosine-phosphorylation of CRKL may be used
CC as a diagnostic indicator for BCL/ABL activity in Ph-positive
CC leukaemia. Thus, overexpression of tyrosine-phosphorylated CRKL
CC protein, or an increase in protein, gene copy number or mRNA is
CC indicative of Ph-positive leukaemia. Fragments of the CRKL protein
CC may also be used in the treatment of individuals with cancers
CC arising from cells which express the CRKL protein by inhibition of
CC the synthesis or activity of the CRKL protein.
SQ Sequence 303 AA;

RESULT 14

```

ID      R71910 standard; Protein; 466 AA.
AC      R71910;
DT      25-SEP-1995 (first entry)
DE      Erythroid p55.
KW      Erythroid p55; erythrocyte membrane protein; hemolytic anemia;
KW      Dyskeratosis congenita; cancer; diagnosis; therapy.
OS      Homo sapiens.
FH      Key                      Location/Qualifiers
FT      Region                    163..233
FT      /label= SH3_motif
FT      Domain                    267..420
FT      /label= Guanylate-kinase
PN      US5401835-A.
PD      28-MAR-1995.
PF      31-JUL-1992; 923739.
PR      31-JUL-1992; US-923739.
PA      (CHIS/) CHISHTI A H.
PI      Chishti AH;
DR      WPI; 95-138985/18.
DR      N-PSDB; Q87925.
PT      New human erythroid p55 nucleic acids - used to develop products
PT      for diagnosis and treatment of p55 abnormalities, and for cancer
PT      treatment
PS      Claim 1; Column 23-28; 31pp; English.
CC      A human reticulocyte lambda-gt11 cDNA library was screened using
CC      rabbit polyclonal antibodies against purified native p55. Positive
CC      plaques were purified and phage DNA was analyzed and used to prepare
CC      probes. Human erythrocyte plasma membrane extracts were analyzed to
CC      obtain DNA (given in Q87925) encoding p55 (R71910).
SQ      Sequence 466 AA;

```

Db 180 keaglkfatgdiiqiinkddsnwqgrvegsskesaglipspelpew 226
| : | | | | : : : | | : | : : | : :
Qy 63 KPGELAFRKGDDVVTILEACENKSWY-RVKHHTSGQEGLLAAGALRER 108

RESULT 15

ID R31046 standard; Protein; 475 AA.
AC R31046;
DT 26-MAY-1993 (first entry)
DE Rat D1B dopamine receptor.
KW PCR; amplify; degenerate; primer; TM; transmembrane region; human; D1;
KW dopamine; receptor; probe; rat; pBLUESCRIPT II SK+; testis; DR5; D1B;
KW genomic library; lambdaDASH II; Kozak; consensus sequence; V-15.
OS Rattus rattus.
PN W09218533-A.
PD 29-OCT-1992.
PF 16-APR-1992; U03187.
PR 16-APR-1991; US-686591.
PA (UYDU-) UNIV DUKE.
PI Caron MG, Jarvie KR, Tiberi M;
DR WPI; 93-036060/04.
DR N-PSDB; Q35148.
PT Cloned gene encoding rat D1b dopamine receptor - used to screen
PT cpds. for receptor activity or in receptor binding assays
PS Disclosure; Page 25-28; 39pp; English.
CC This sequence represents rat D1B dopamine receptor. The DNA
CC sequence encoding this polypeptide was isolated using the primer
CC sequences given in Q35146-47. These oligomers are degenerate primers
CC corresponding to the 5th and 6th transmembrane (TM) regions of the
CC human D1 dopamine receptor. These primers were used to amplify
CC sheared human DNA and the amplification products were subcloned into
CC the sequencing vector pBLUESCRIPT II SK+. A 230bp fragment (V-15) was
CC found to correspond to the 5th TM region, the 3rd intracellular loop
CC and the 6th TM region. V-15 was used as a template for the synthesis
CC of a 32P-labeled probe. This probe was used to screen a rat testis
CC genomic library in lambdaDASH II. One isolated clone (DR5) had an
CC open reading frame of 1425 bp (475 amino acids) which contained the
CC full coding sequence for rat D1B-dopamine receptor. The predicted
CC encoded protein has a molecular weight of 52834. The putative
CC initiator methionine was selected on the basis of the best Kozak
CC consensus sequence found in frame with the remainder of the coding
CC block and preceded by a stop codon.
SQ Sequence 475 AA;

Query Match 17.5%; Score 81; DB 6; Length 475;
Best Local Similarity 47.8%; Pred. No. 2.86e+00;
Matches 11; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 177 nuhrdkagsqgqegllsngtpwe 199
: | | | : | | | | : | : |
Qy 85 SWYRVKHHTSGQEGLLAAGALRE 107

Search completed: Mon Feb 3 16:52:22 1997
Job time : 12 secs.

W09218533-A (TM)

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 16:51:25 1997; MasPar time 4.09 Seconds
 402.449 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-2
 Description: (48-111) from US08426509.pep (1 of 4)
 Perfect Score: 464
 Sequence: 1 APGTQCITKCEHTRPKPGEL.....HTSGQEGLLAAGALREREAL 64

Scoring table: PAM 150
 Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: pir48
 1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
 14:unrev

Statistics: Mean 35.059; Variance 66.115; scale 0.530

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description	Pred. No.
			%					
1	464	100.0	507	4	A55625	protein-tyrosine kin	7.24e-76	
2	449	96.8	527	11	A49865	protein-tyrosine kin	1.16e-72	
3	420	90.5	465	4	B55625	protein-tyrosine kin	1.72e-66	
4	403	86.9	465	12	I48926	protein-tyrosine kin	6.85e-63	
5	165	35.6	450	4	A41973	protein-tyrosine kin	7.64e-15	
6	161	34.7	450	12	I48929	protein-tyrosine kin	4.17e-14	
7	161	34.7	450	1	S15094	protein-tyrosine kin	4.17e-14	
8	161	34.7	450	1	JH0559	protein-tyrosine kin	4.17e-14	
9	125	26.9	468	10	S46791	hypothetical protein	1.02e-07	
10	116	25.0	211	10	A46444	SH2-SH3 adaptor prot	3.33e-06	
11	115	24.8	217	11	JT0664	growth factor recept	4.88e-06	
12	113	24.4	217	12	A54688	modular adaptor Grb2	1.04e-05	
13	113	24.4	217	12	S26050	gene ash protein - r	1.04e-05	
14	113	24.4	217	11	A43321	growth factor recept	1.04e-05	
15	112	24.1	2415	10	A33733	spectrin alpha chain	1.52e-05	
16	111	23.9	451	10	S58653	hypothetical protein	2.21e-05	
17	110	23.7	452	10	S46798	hypothetical protein	3.22e-05	
18	110	23.7	505	4	S24550	protein-tyrosine kin	3.22e-05	
19	110	23.7	506	4	S24553	protein-tyrosine kin	3.22e-05	
20	102	22.0	228	10	S25730	sen-5 protein - Caen	6.12e-04	
21	102	22.0	527	12	A55631	protein-tyrosine kin	6.12e-04	
22	100	21.6	512	4	A39719	protein-tyrosine kin	1.26e-03	
23	100	21.6	620	4	S33253	protein-tyrosine kin	1.26e-03	
24	99	21.3	442	11	A45184	B cell progenitor ki	1.80e-03	
25	98	21.1	507	4	A39939	protein-tyrosine kin	2.57e-03	

26	98	21.1	821	12	S39983	eps8 protein - mouse	2.57e-03
27	97	20.9	968	12	S46992	protein p130 - rat	3.67e-03
28	97	20.9	2429	2	SJHUA	spectrin alpha chain	3.67e-03
29	96	20.7	467	14	A57627	p55 erythrocyte memb	5.22e-03
30	95	20.5	509	4	A23639	protein-tyrosine kin	7.42e-03
31	95	20.5	509	1	OKHULK	protein-tyrosine kin	7.42e-03
32	95	20.5	659	11	I37212	Bruton agammaglobuli	7.42e-03
33	95	20.5	659	12	B45184	B cell progenitor ki	7.42e-03
34	95	20.5	659	11	S28912	protein-tyrosine kin	7.42e-03
35	95	20.5	660	12	JN0471	protein-tyrosine kin	7.42e-03
36	92	19.8	512	1	TVHULY	protein-tyrosine kin	2.11e-02
37	89	19.2	303	5	S41754	CRKL protein - human	5.87e-02
38	88	19.0	1244	9	S25327	cytoskeleton assembl	8.23e-02
39	87	18.8	377	11	S08636	nck protein - human	1.15e-01
40	87	18.8	532	4	B34104	protein-tyrosine kin	1.15e-01
41	87	18.8	534	4	A44991	protein-tyrosine kin	1.15e-01
42	87	18.8	534	4	S33568	protein-tyrosine kin	1.15e-01
43	87	18.8	537	1	TVHUSR	protein-tyrosine kin	1.15e-01
44	87	18.8	537	1	TVHUSY	protein-tyrosine kin	1.15e-01
45	87	18.8	1099	11	S31926	myosin 1B heavy chai	1.15e-01

ALIGNMENTS

RESULT 1

ENTRY A55625 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112),
megakaryocyte-associated - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
01-Mar-1996

ACCESSIONS A55625; S43533

REFERENCE A55625

#authors Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,
L.L.; White, R.A.; Avraham, H.

#journal J. Biol. Chem. (1995) 270:1833-1842

#title Structural and functional studies of the intracellular
tyrosine kinase MATK gene and its translated product.

#accession A55625

##status preliminary; not compared with conceptual translation

##molecule_type DNA

##residues 1-507 ##label AVR

REFERENCE S43533

#authors Sakano, S.; Iwama, A.; Inazawa, J.; Ariyama, T.; Ohno, M.;
Suda, T.

#journal Oncogene (1994) 9:1155-1161

#title Molecular cloning of a novel non-receptor tyrosine kinase,
HYL (hematopoietic consensus tyrosine-lacking kinase).

#accession S43533

##status preliminary

##molecule_type mRNA

##residues 1-507 ##label SAK

##cross-references EMBL:X77278

GENETICS

#gene GDB:MATK

##cross-references GDB:G00-304-667

CLASSIFICATION #superfamily SH2 homology; protein kinase homology; SH3
homology

KEYWORDS phosphotransferase

FEATURE

55-105 #domain SH3 homology #label SH31\

122-211 #domain SH2 homology #label SH2\

233-485 #domain protein kinase homology #label KIN

SUMMARY #length 507 #molecular-weight 56469 #checksum 6051

Query Match 100.0%; Score 464; DB 4; Length 507;

Best Local Similarity 100.0%; Pred. No. 7.24e-76;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 48 apgtqcitkcehtrpkpgelafrkgdvvtileacenkswyrvkhhtsgqegllaagalre 107
|||||
Qy 48 APTQCITKCENTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRE 107

Db 108 real 111
||||
Qy 108 REAL 111

RESULT 2

ENTRY A49865 #type complete
TITLE protein-tyrosine kinase (EC 2.7.1.112) mtk - human
ALTERNATE_NAMES megakaryocyte-associated tyrosine kinase
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change
19-Oct-1995
ACCESSIONS A49865
REFERENCE A49865
#authors Bennett, B.D.; Cowley, S.; Jiang, S.; London, R.; Deng, B.;
Grabarek, J.; Groopman, J.E.; Goeddel, D.V.; Avraham, H.
#journal J. Biol. Chem. (1994) 269:1068-1074
#title Identification and characterization of a novel tyrosine
kinase from megakaryocytes.
#accession A49865
##status preliminary
##molecule_type mRNA
##residues 1-527 ##label BEN
##cross-references GB:L18974
CLASSIFICATION #superfamily SH2 homology; protein kinase homology; SH3
homology
KEYWORDS phosphotransferase
FEATURE
55-105 #domain SH3 homology #label SH31\
122-211 #domain SH2 homology #label SH2\
233-484 #domain protein kinase homology #label KIN
SUMMARY #length 527 #molecular-weight 58473 #checksum 1630

Query Match 96.8%; Score 449; DB 11; Length 527;
Best Local Similarity 96.9%; Pred. No. 1.16e-72;
Matches 62; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 48 apgtqcitkcehtrpkpgelafrkgdvvtileacenkswyrvkhhtsgqegllaagalrd 107
|||||
Qy 48 APTQCITKCENTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRE 107

Db 108 geal 111
|||
Qy 108 REAL 111

RESULT 3

ENTRY B55625 #type complete
TITLE protein-tyrosine kinase (EC 2.7.1.112),
megakaryocyte-associated - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
19-Oct-1995
ACCESSIONS B55625
REFERENCE A55625
#authors Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,
L.L.; White, R.A.; Avraham, H.
#journal J. Biol. Chem. (1995) 270:1833-1842
#title Structural and functional studies of the intracellular

tyrosine kinase MATK gene and its translated product.

#accession B55625
##status preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues 1-465 ##label AVR
CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2
homology
KEYWORDS phosphotransferase
FEATURE
13-63 #domain SH3 homology #label SH31\
80-169 #domain SH2 homology #label SH2\
191-443 #domain protein kinase homology #label KIN
SUMMARY #length 465 #molecular-weight 51585 #checksum 6919

Query Match 90.5%; Score 420; DB 4; Length 465;
Best Local Similarity 85.9%; Pred. No. 1.72e-66;
Matches 55; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 6 apgtqcnkcnsrcpkipgelafkrkgdvtileacedksyrrakhhgsgqegllaaaalrq 65
|||||:||||:|||||||||||:||||||:|||| ||| |||||||||:||||
Qy 48 APGTQCITKCENTRKPGEAFRKGDVVTILEACENKSWYRVKHHHTSGQEGLLAAGALRE 107

Db 66 real 69
||||
Qy 108 REAL 111

RESULT 4

ENTRY I48926 #type complete
TITLE protein-tyrosine kinase (EC 2.7.1.112) Ctk - mouse
ALTERNATE_NAMES csk-type protein-tyrosine kinase
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change
15-Mar-1996
ACCESSIONS I48926
REFERENCE A53469
#authors Klages, S.; Adam, D.; Class, K.; Fargnoli, J.; Bolen, J.B.;
Penhallow, R.C.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2597-2601
#title Ctk: a protein-tyrosine kinase related to Csk that defines an
enzyme family.
#cross-references MUID:94195789
#accession I48926
##status preliminary
##molecule_type mRNA
##residues 1-465 ##label RES
##cross-references EMBL:U05210; NID:g450232; CDS_PID:g450233
KEYWORDS phosphotransferase
SUMMARY #length 465 #molecular-weight 51495 #checksum 6748

Query Match 86.9%; Score 403; DB 12; Length 465;
Best Local Similarity 84.4%; Pred. No. 6.85e-63;
Matches 54; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 6 apgtqcnkcnsrcpkipgelafkrkgdvtileacedksyrrakhhgsgqegllaaaalrh 65
|||||:||||:|||||||||||:||||||:|||| ||| |||||||||:||||
Qy 48 APGTQCITKCENTRKPGEAFRKGDVVTILEACENKSWYRVKHHHTSGQEGLLAAGALRE 107

Db 66 geal 69
|||
Qy 108 REAL 111

RESULT 5

ENTRY A41973 #type fragment
TITLE protein-tyrosine kinase (EC 2.7.1.112) CSK - chicken

```

Db      415 eeitllkelgsgqfgvvqlgkukggydvavkniegsmsedefqeaqtamklsphklvk 474
      : || :| | | | | | | | | | : : : | : | :| :
Qy      233 QHLTLGAQIGEGEFGAVLQGEYLGQ-KVAVKNIK-CDVTAQAFLETAVMTKMQHENLVR 290

Db      475 fygvcscopyiyivteyisngcllnylrshgkgl-epsqllcmcydvcegnafleshqfi 533
      : || : :| | | :| :| | :| :| :| : : :| | | :| | : :
Qy      291 LLGVILHQ-GLYIVMEHVSCKNLVNFRLTRGRALVNTAQLLQFSLHVAEGMEYLESKKLV 349


Db      534 hrdlaarncldrdclcvkvsdfgmtryvlddqyvsstvgtkfpvkwsapevfhyfkyssks 593
      || || || || || || : : : : | : : || || : | : ||
Qy      350 HRDLAARNILVSEDLVAKVSDFLAK-A-ERKGLDS--SRLPVKWTAPEALKHGKFTSKS 405

Db      594 dvwafgilawefslgkqpydydndsqvvlkvsqghrlyrphlasdtiyqinyscuhelp 653
      || :| :| :| || | : | | : | : : :| || |
Qy      406 DVWSFGVLLWEVFSYGRAPYPKMSLKEVSEAVEKGYRMEPPEGCPGVHVMSSCWEAEP 465

Db      654 ekrptfqql 662
      : || | : |
Qy      466 ARPPFRKL 474

```

[illegible]


 (TM)

```

NPsrch_pp    protein - protein database search, using Smith-Waterman algorithm
Run on:      Mon Feb  3 16:57:28 1997;  MasPar time 9.41 Seconds
              672.791 Million cell updates/sec
Tabular output not generated.

```

Scoring table: PAM 150
Gap 11

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir48
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4

Statistics: Mean 45.505; Variance 121.033; scale 0.376

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query		Z		DB	ID	Description	Pred. No.
No.	Score	Match	Length	DB	ID				
1	1798	100.0	507	4	A55625			protein-tyrosine kin	3.01e-257
2	1730	96.2	465	4	B55625			protein-tyrosine kin	2.05e-246
3	1730	96.2	465	12	I48926			protein-tyrosine kin	2.05e-246
4	1683	93.6	527	11	A49865			protein-tyrosine kin	6.22e-239
5	1160	64.5	450	4	A41973			protein-tyrosine kin	3.91e-156
6	1148	63.8	450	1	JH0559			protein-tyrosine kin	3.01e-154
7	1145	63.7	450	1	S15094			protein-tyrosine kin	8.92e-154
8	1125	62.6	450	12	I48929			protein-tyrosine kin	1.24e-150
9	838	46.6	507	4	A39939			protein-tyrosine kin	7.94e-106
10	837	46.6	1520	1	TVFFA			protein-tyrosine kin	1.14e-105
11	821	45.7	542	11	A49114			protein-tyrosine kin	3.41e-103
12	817	45.4	509	1	OKHULK			protein-tyrosine kin	1.42e-102
13	816	45.4	1146	4	B35962			protein-tyrosine kin	2.03e-102
14	816	45.4	1182	4	A35962			protein-tyrosine kin	2.03e-102
15	814	45.3	557	10	A00629			protein-tyrosine kin	4.13e-102
16	812	45.2	697	7	A26132			gag-abl-pol polyprot	8.43e-102
17	812	45.2	1130	1	TVHUA			protein-tyrosine kin	8.43e-102
18	811	45.1	505	1	TVHUHC			protein-tyrosine kin	1.20e-101
19	809	45.0	526	4	S20808			protein-tyrosine kin	2.45e-101
20	808	44.9	981	1	F0NVGM			gag-abl polyprotein	3.50e-101
21	808	44.9	1123	4	A39962			kinase-related trans	3.50e-101
22	803	44.7	509	4	A23639			protein-tyrosine kin	2.08e-100
23	804	44.7	526	7	S26420			src protein - Rous s	1.45e-100
24	804	44.7	526	7	S20676			protein-tyrosine kin	1.45e-100
25	803	44.7	526	1	OKFVVR			protein-tyrosine kin	2.08e-100
26	803	44.7	536	4	S33569			protein-tyrosine kin	2.08e-100
27	802	44.6	526	1	TVFVVR			protein-tyrosine kin	2.97e-100
28	800	44.5	537	4	A43806			protein-tyrosine kin	6.04e-100
29	799	44.4	537	1	TVHUSY			protein-tyrosine kin	8.63e-100
30	799	44.4	541	1	TVCHYS			protein-tyrosine kin	8.63e-100
31	799	44.4	568	1	TVFVS1			protein-tyrosine kin	8.63e-100
32	796	44.3	528	1	TVFVG9			protein-tyrosine kin	2.51e-99
33	794	44.2	526	4	S15582			protein-tyrosine kin	5.11e-99
34	794	44.2	533	1	TVCHS			protein-tyrosine kin	5.11e-99
35	793	44.1	537	1	TVHUSR			protein-tyrosine kin	7.29e-99
36	793	44.1	539	11	B49114			protein-tyrosine kin	7.29e-99
37	792	44.0	503	4	J01321			protein-tyrosine kin	1.04e-98
38	792	44.0	523	1	TVFVMT			protein-tyrosine kin	1.04e-98
39	791	44.0	526	1	TVFV60			protein-tyrosine kin	1.49e-98
40	791	44.0	542	1	TVHUSC			protein-tyrosine kin	1.49e-98
41	792	44.0	543	1	TVHUYS			protein-tyrosine kin	1.04e-98
42	791	44.0	557	1	TVFVS2			protein-tyrosine kin	1.49e-98
43	791	44.0	587	1	TVFVPR			protein-tyrosine kin	1.49e-98
44	792	44.0	590	1	TVFFDS			protein-tyrosine kin	1.04e-98
45	790	43.9	541	4	A43610			protein-tyrosine kin	2.12e-98

ALIGNMENTS

RESULT 1
ENTRY A55625 #type complete
TITLE protein-tyrosine kinase (EC 2.7.1.112),

ORGANISM megakaryocyte-associated - human
 #formal_name Homo sapiens #common_name man
 DATE 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
 01-Mar-1996
 ACCESSIONS A55625; S43533
 REFERENCE A55625
 #authors Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,
 L.L.; White, R.A.; Avraham, H.
 #journal J. Biol. Chem. (1995) 270:1833-1842
 #title Structural and functional studies of the intracellular
 tyrosine kinase MATK gene and its translated product.
 #accession A55625
 ##status preliminary; not compared with conceptual translation
 ##molecule_type DNA
 ##residues 1-507 ##label AVR
 REFERENCE S43533
 #authors Sakano, S.; Iwama, A.; Inazawa, J.; Ariyama, T.; Ohno, M.;
 Suda, T.
 #journal Oncogene (1994) 9:1155-1161
 #title Molecular cloning of a novel non-receptor tyrosine kinase,
 HYL (hematopoietic consensus tyrosine-lacking kinase).
 #accession S43533
 ##status preliminary
 ##molecule_type mRNA
 ##residues 1-507 ##label SAK
 ##cross-references EMBL:X77278
 GENETICS
 #gene GDB:MATK
 ##cross-references GDB:G00-304-667
 CLASSIFICATION #superfamily SH2 homology; protein kinase homology; SH3
 homology
 KEYWORDS phosphotransferase
 FEATURE
 55-105 #domain SH3 homology #label SH31\
 122-211 #domain SH2 homology #label SH2\
 233-485 #domain protein kinase homology #label KIN
 SUMMARY #length 507 #molecular-weight 56469 #checksum 6051

Query Match 100.0%; Score 1798; DB 4; Length 507;
 Best Local Similarity 100.0%; Pred. No. 3.01e-257;
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   233 qhltlgaqigegefgavlqgeylgqkvavknikcdvtaqafldetavtnkqhnlvrll 292
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Db   293 gvilhqglyivnehvskgnlnvflrtrgralvntaqlqlqfslhvaeagneyleskklvhrd 352
      |||
Gy   293 GVILHQGLYIVMEHVSKGNLVNFLRTRGRALVNTAQLQLQFSLHVAEGMEYLESKKLVHRD 352

Db   353 laarnilvsedlvakvsdfglakaerkgldssrlpvkwtapealkhkgftsksdvwsfgv 412
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Gy   353 LAARNILVSEDLVAKVSDFGLAKAERKGLDSSRLPVKWTAPEALKHKGFTSKSDVWSFGV 412

Db   413 llwevfsygrapypknsikevseavekgyrneppegcpgpvhvlmsscweaeparrppfr 472
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Gy   413 LLWEVFSYGRAPYPKNSLKEVSEAVEKGYRNEPPEGCPGPVHVLMSSCWEAEPARRPPFR 472

Db   473 klaekl 478
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Gy   473 KLAEKL 478
  
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RESULT 2
 ENTRY B55625 #type complete
 TITLE protein-tyrosine kinase (EC 2.7.1.112),

ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
 19-Oct-1995
 ACCESSIONS B55625
 REFERENCE A55625
 #authors Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,
 L.L.; White, R.A.; Avraham, H.
 #journal J. Biol. Chem. (1995) 270:1833-1842
 #title Structural and functional studies of the intracellular
 tyrosine kinase MATK gene and its translated product.
 #accession B55625
 ##status preliminary; not compared with conceptual translation
 ##molecule_type mRNA
 ##residues 1-465 ##label AVR
 CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2
 homology
 KEYWORDS phosphotransferase
 FEATURE
 13-63 #domain SH3 homology #label SH31\
 80-169 #domain SH2 homology #label SH2\
 191-443 #domain protein kinase homology #label KIN
 SUMMARY #length 465 #molecular-weight 51585 #checksum 6919

Query Match 96.2%; Score 1730; DB 4; Length 465;
 Best Local Similarity 93.9%; Pred. No. 2.05e-246;
 Matches 231; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Db 191 qhltlgaqigegefgavlqgeylgqkvavknikcdvtaqafldetavmtklqhrnlvrll 250
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 Qy 233 QHLLTGAQIGEGEFGAVLQGEYLGQKVAVKNIKCDVTAQAFLDETAVMTKMQHENVRL 292
 Db 251 gvilhhglyivnehvskgnlvnflrtrgralvstsqllqfalhvaeqmeyleskklvhrd 310
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 Db 311 laarnilvsedlvakvsdfglakaerkgldssrlpvkwtapealkngrfssksdvwsfgv 370
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 Qy 353 LAARNILVSEDLVAKVSDFGLAKAERKGLDSSRLPVKWTAPEALKHGKFTSKSDVWSFGV 412
 Db 371 llwevfsygrapypknsлкеvseavekgyrneppdgcpgsvhtlmgscweaeparrppfr 430
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 Qy 413 LLWEVFSYGRAPYPKNSLKEVSEAVEKGYRNEPPEGCPGVHVLSSCWEAEPARRPPFR 472
 Db 431 kivekl 436
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 Qy 473 KLAEKL 478

RESULT 3
 ENTRY 148926 #type complete
 TITLE protein-tyrosine kinase (EC 2.7.1.112) Ctk - mouse
 ALTERNATE_NAMES csk-type protein-tyrosine kinase
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change
 15-Mar-1996
 ACCESSIONS I48926
 REFERENCE A53469
 #authors Klages, S.; Adam, D.; Class, K.; Fargnoli, J.; Bolen, J.B.;
 Penhallow, R.C.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2597-2601
 #title Ctk: a protein-tyrosine kinase related to Csk that defines an
 enzyme family.
 #cross-references MUID:94195789
 #accession I48926
 ##status preliminary

##molecule_type mRNA
##residues 1-465 ##label RES
##cross-references EMBL:U05210; NID:g450232; CDS_PID:g450233

KEYWORDS phosphotransferase

SUMMARY #length 465 #molecular-weight 51495 #checksum 6748

Query Match 96.2%; Score 1730; DB 12; Length 465;
Best Local Similarity 93.9%; Pred. No. 2.05e-246;
Matches 231; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Db 191 qhltlgaqigegefgavlqgeylgqkvavknikcdvtaqafldetavatkqhnrnlvrll 250
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Qy 233 QHLTLGAQIGEGEFGAVLQGEYLGQKVAVKNIKCDVTAQAFLETAVMTKMQHENLVRL 292

Db 251 gvilhhglyivnehvskgnlvnflrtrgralvstsqllqfalhvaegmeyleskklvhrd 310
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Qy 293 GVILHGGLYIVNEHVSKGNLVNFLRTRGRALVNTAQLLQFSLHVAEGMEYLESKKLVRD 352

Db 311 laarnilvsedlvakvsdfglakaerkgldssrlpvkwtapealkngrfssksdvsfsgv 370
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Qy 353 LAARNILVSEDLVAKVSDFGLAKAERKGLDSSRLPVKWTAPEALKHGKFTSKSDVWSFGV 412

Db 371 lluevfsygrapykmslkeakseavekgyrneppdgcpvhlmgscweaeparrppfr 430
|||||
Qy 413 LLUEVFSYGRAPYPKMSLKEVSEAVEKGYRMEPPEGCPGVHVMSSCWEAEPARRPPFR 472

Db 431 kivekl 436
|: |||
Qy 473 KLAEKL 478

RESULT 4

ENTRY A49865 #type complete
TITLE protein-tyrosine kinase (EC 2.7.1.112) natk - human
ALTERNATE_NAMES megakaryocyte-associated tyrosine kinase
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change
19-Oct-1995
ACCESSIONS A49865
REFERENCE A49865
#authors Bennett, B.D.; Cowley, S.; Jiang, S.; London, R.; Deng, B.;
Grabarek, J.; Groopman, J.E.; Goeddel, D.V.; Avraham, H.
#journal J. Biol. Chem. (1994) 269:1068-1074
#title Identification and characterization of a novel tyrosine
kinase from megakaryocytes.
#accession A49865
##status preliminary
##molecule_type mRNA
##residues 1-527 ##label BEN
##cross-references GB:L18974
CLASSIFICATION #superfamily SH2 homology; protein kinase homology; SH3
homology
KEYWORDS phosphotransferase
FEATURE
55-105 #domain SH3 homology #label SH31\
122-211 #domain SH2 homology #label SH2\
233-484 #domain protein kinase homology #label KIN
SUMMARY #length 527 #molecular-weight 58473 #checksum 1630

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Best Local Similarity 99.1%; Pred. No. 6.22e-239;
Matches 232; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Db 233 qhltlgaqigegefgavlqgeylgqkvavknikcdvtaqafldetavatkqhnrnlvrll 292
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Db      293  gvilhgglyivnehvskgnlvnflrtrgralvntaqlqfslhvaegmeyleskklvhrd 352
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Qy      293  GVILHGGLYIVMEHVS KGNLVNFLRTRGRALVNTAQLQFSLHVAEGMEYLESKKLVHRD 352

Db      353  laarnilvsedlvakvsdfglakaerkgldssrtpvkwtapealkhg-ftsksdvsfvg 411
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Qy      353  LAARNILVSEDLVAKVSD FGLAKAERKGLDSSRLPVKWTAPEALKHCKFTSKSDVVSFGV 412

Db      412  llwevfsgyrapypkns lkevs eavekgyrnepegcpgpvhvlmsscweaepp 465
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Qy      413  LLWEVFSYGRAPYPKNS LKEVSEAVEKGYRNEPEGCPGPVHVLMSSCWEAEPA 466

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RESULT 5

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ENTRY          A41973      #type fragment
TITLE          protein-tyrosine kinase (EC 2.7.1.112) CSK - chicken
                (fragment)
ORGANISM       #formal_name Gallus gallus #common_name chicken
DATE          31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                12-Apr-1995
ACCESSIONS     A41973
REFERENCE      A41973
#authors       Sabe, H.; Knudsen, B.; Okada, M.; Nada, S.; Nakagawa, H.;
                Hanafusa, H.
#journal       Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2190-2194
#title         Molecular cloning and expression of chicken C-terminal Src
                kinase: lack of stable association with c-Src protein.
#cross-references MUID:92196083
#accession     A41973
##status       preliminary
##molecule_type DNA
##residues     1-450 ##label SAB
##cross-references NCBIN:88058; NCBIP:88059
##note         sequence extracted from NCBI backbone
CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase
                homology; SH2 homology; SH3 homology
KEYWORDS       ATP; phosphotransferase; tyrosine-specific protein kinase
FEATURE
16-65          #domain SH3 homology #label SH3\
82-171         #domain SH2 homology #label SH2\
193-447        #domain protein kinase homology #label KIN\
201-209        #region protein kinase ATP-binding motif
SUMMARY        #length 450 #checksum 7
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Query Match 64.5%; Score 1160; DB 4; Length 450;
Best Local Similarity 59.3%; Pred. No. 3.91e-156;
Matches 146; Conservative 50; Mismatches 48; Indels 2; Gaps 1;

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Db      195 lklqliigkgefgdvalgdyrgnkavaykcikndataqaf laeasvntqlrhnslvqllgv 254  
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Qy      235 LTlGAQIGEGEFGAVLQGEYLGQKVAVKNIKCDVTAQAFLDetaVNTKMQHENLVRL LGV 294  
  
Db      255 iveeksglyivteymakgslvdylrsgrsvlggdcilkfslvceameyleannfvhrd 314  
       | : : | | | | | : : | : | : | : | : | : | | | | | : : : | | |  
Qy      295 ILHQ--GLYIVMEHVSKGNLVNFLRTRGRALVNTAQLLQFSLHVAEGMEYLESKKLVHRD 352  
  
Db      315 laarnvlvsedniakvsdfgltk easstqdtgklpvkutapealrekkfstksdvwsfgi 374  
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Db      375 llweiyfsgrvpypriplkdvvprvekgykadppdgcpaiyvgevakkcwtldpghrpsfh 434  
       | | | : : | : | | | : : | : | | | | | : | : | | | : | : | : | : | : | : | :  
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Db      435 alreal 440
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Release 2.1D John F. Collins, Biocomputing Research Unit.
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